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SEQUENCE LISTING

<110> Haseltine et al.

<120> Human DNA Mismatch Repair Proteins

<130> PF106P3D1

<140> 10/079,429

<141> 2002-02-22

<150> PCT/US95/01035

<151> 1995-01-25

<150> 08/468,024

<151> 1995-06-06

<150> 08/465,679

<151> 1995-06-06

<150> 08/294,312

<151> 1994-08-23

<150> 08/210,143

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<150> 08/187,757

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<160> 78

<170> PatentIn version 3.0

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tcc caa att gaa aaa aga agg agt caa aat att aaa atg gta cag atc Ser Gln Ile Glu Lys Arg Arg Ser Gln Asn Ile Lys Met Val Gln Ile 685 690 695			2177
ccc ttt tct atg aaa aac tta aaa ata aat ttt aag aaa caa aac aaa Pro Phe Ser Met Lys Asn Leu Lys Ile Asn Phe Lys Lys Gln Asn Lys 700 705 710 715			2225
gtt gac tta gaa gag aag gat gaa cct tgc ttg atc cac aat ctc agg Val Asp Leu Glu Glu Lys Asp Glu Pro Cys Leu Ile His Asn Leu Arg 720 725 730			2273
ttt cct gat gca tgg cta atg aca tcc aaa aca gag gta atg tta tta Phe Pro Asp Ala Trp Leu Met Thr Ser Lys Thr Glu Val Met Leu Leu 735 740 745			2321
aat cca tat aga gta gaa gaa gcc ctg cta ttt aaa aga ctt ctt gag Asn Pro Tyr Arg Val Glu Glu Ala Leu Leu Phe Lys Arg Leu Leu Glu 750 755 760			2369
aat cat aaa ctt cct gca gag cca ctg gaa aag cca att atg tta aca Asn His Lys Leu Pro Ala Glu Pro Leu Glu Lys Pro Ile Met Leu Thr 765 770 775			2417
gag agt ctt ttt aat gga tct cat tat tta gac gtt tta tat aaa atg Glu Ser Leu Phe Asn Gly Ser His Tyr Leu Asp Val Leu Tyr Lys Met 780 785 790 795			2465
aca gca gat gac caa aga tac agt gga tca act tac ctg tct gat cct Thr Ala Asp Asp Gln Arg Tyr Ser Gly Ser Thr Tyr Leu Ser Asp Pro			2513

	800	805	810	
	cgt ctt aca gcg aat ggt ttc aag ata aaa ttg ata cca gga gtt tca			2561
	Arg Leu Thr Ala Asn Gly Phe Lys Ile Lys Leu Ile Pro Gly Val Ser			
	815	820	825	
	att act gaa aat tac ttg gaa ata gaa gga atg gct aat tgt ctc cca			2609
	Ile Thr Glu Asn Tyr Leu Glu Ile Glu Gly Met Ala Asn Cys Leu Pro			
	830	835	840	
	ttc tat gga gta gca gat tta aaa gaa att ctt aat gct ata tta aac			2657
	Phe Tyr Gly Val Ala Asp Leu Lys Glu Ile Leu Asn Ala Ile Leu Asn			
	845	850	855	
	aga aat gca aag gaa gtt tat gaa tgt aga cct cgc aaa gtg ata agt			2705
	Arg Asn Ala Lys Glu Val Tyr Glu Cys Arg Pro Arg Lys Val Ile Ser			
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	tat tta gag gga gaa gca gtg cgt cta tcc aga caa tta ccc atg tac			2753
	Tyr Leu Glu Gly Glu Ala Val Arg Leu Ser Arg Gln Leu Pro Met Tyr			
	880	885	890	
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	Leu Ser Lys Glu Asp Ile Gln Asp Ile Ile Tyr Arg Met Lys His Gln			
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	Phe Gly Asn Glu Ile Lys Glu Cys Val His Gly Arg Pro Phe Phe His			
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	His Leu Thr Tyr Leu Pro Glu Thr Thr			
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	tgtattatgt gtcacatggt tatttttttaa atgaggattc actgacttgt ttttatattg			3019
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Phe Asp Lys Ile Glu Val Arg Asp Asn Gly Glu Gly Ile Lys Ala Val
50 55 60

Asp Ala Pro Val Met Ala Met Lys Tyr Tyr Thr Ser Lys Ile Asn Ser
65 70 75 80

His Glu Asp Leu Glu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala
85 90 95

Leu Gly Ser Ile Cys Cys Ile Ala Glu Val Leu Ile Thr Thr Arg Thr
100 105 110

Ala Ala Asp Asn Phe Ser Thr Gln Tyr Val Leu Asp Gly Ser Gly His
115 120 125

Ile Leu Ser Gln Lys Pro Ser His Leu Gly Gln Gly Thr Thr Val Thr
130 135 140

Ala Leu Arg Leu Phe Lys Asn Leu Pro Val Arg Lys Gln Phe Tyr Ser
145 150 155 160

Thr Ala Lys Lys Cys Lys Asp Glu Ile Lys Lys Ile Gln Asp Leu Leu
165 170 175

Met Ser Phe Gly Ile Leu Lys Pro Asp Leu Arg Ile Val Phe Val His
180 185 190

Asn Lys Ala Val Ile Trp Gln Lys Ser Arg Val Ser Asp His Lys Met
195 200 205

Ala Leu Met Ser Val Leu Gly Thr Ala Val Met Asn Asn Met Glu Ser
210 215 220

Phe Gln Tyr His Ser Glu Glu Ser Gln Ile Tyr Leu Ser Gly Phe Leu
225 230 235 240

Pro Lys Cys Asp Ala Asp His Ser Phe Thr Ser Leu Ser Thr Pro Glu
245 250 255

Arg Ser Phe Ile Phe Ile Asn Ser Arg Pro Val His Gln Lys Asp Ile
260 265 270

Leu Lys Leu Ile Arg His His Tyr Asn Leu Lys Cys Leu Lys Glu Ser
275 280 285

Thr Arg Leu Tyr Pro Val Phe Phe Leu Lys Ile Asp Val Pro Thr Ala
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Asp Val Asp Val Asn Leu Thr Pro Asp Lys Ser Gln Val Leu Leu Gln
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Asn Lys Glu Ser Val Leu Ile Ala Leu Glu Asn Leu Met Thr Thr Cys
 325 330 335

Tyr Gly Pro Leu Pro Ser Thr Asn Ser Tyr Glu Asn Asn Lys Thr Asp
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Val Ser Ala Ala Asp Ile Val Leu Ser Lys Thr Ala Glu Thr Asp Val
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Leu Phe Asn Lys Val Glu Ser Ser Gly Lys Asn Tyr Ser Asn Val Asp
 370 375 380

Thr Ser Val Ile Pro Phe Gln Asn Asp Met His Asn Asp Glu Ser Gly
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Lys Asn Thr Asp Asp Cys Leu Asn His Gln Ile Ser Ile Gly Asp Phe
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Gly Tyr Gly His Cys Ser Ser Glu Ile Ser Asn Ile Asp Lys Asn Thr
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Lys Asn Ala Phe Gln Asp Ile Ser Met Ser Asn Val Ser Trp Glu Asn
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Ser Gln Thr Glu Tyr Ser Lys Thr Cys Phe Ile Ser Ser Val Lys His
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Thr Gln Ser Glu Asn Gly Asn Lys Asp His Ile Asp Glu Ser Gly Glu
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Asn Glu Glu Glu Ala Gly Leu Glu Asn Ser Ser Glu Ile Ser Ala Asp
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Glu Trp Ser Arg Gly Asn Ile Leu Lys Asn Ser Val Gly Glu Asn Ile
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Glu Pro Val Lys Ile Leu Val Pro Glu Lys Ser Leu Pro Cys Lys Val
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Ser Asn Asn Asn Tyr Pro Ile Pro Glu Gln Met Asn Leu Asn Glu Asp
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Ser Cys Asn Lys Lys Ser Asn Val Ile Asp Asn Lys Ser Gly Lys Val
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Ala Ser Ala Leu Phe Val Gln Asp His Arg Pro Gln Phe Leu Ile Glu
 580 585 590

Asn Pro Lys Thr Ser Leu Glu Asp Ala Thr Leu Gln Ile Glu Glu Leu
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Trp Lys Thr Leu Ser Glu Glu Glu Lys Leu Lys Tyr Glu Glu Lys Ala
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Thr Lys Asp Leu Glu Arg Tyr Asn Ser Gln Met Lys Arg Ala Ile Glu
 625 630 635 640

Gln Glu Ser Gln Met Ser Leu Lys Asp Gly Arg Lys Lys Ile Lys Pro
 645 650 655

Thr Ser Ala Trp Asn Leu Ala Gln Lys His Lys Leu Lys Thr Ser Leu
 660 665 670

Ser Asn Gln Pro Lys Leu Asp Glu Leu Leu Gln Ser Gln Ile Glu Lys
 675 680 685

Arg Arg Ser Gln Asn Ile Lys Met Val Gln Ile Pro Phe Ser Met Lys
 690 695 700

Asn Leu Lys Ile Asn Phe Lys Lys Gln Asn Lys Val Asp Leu Glu Glu
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Lys Asp Glu Pro Cys Leu Ile His Asn Leu Arg Phe Pro Asp Ala Trp
 725 730 735

Leu Met Thr Ser Lys Thr Glu Val Met Leu Leu Asn Pro Tyr Arg Val
 740 745 750

Glu Glu Ala Leu Leu Phe Lys Arg Leu Leu Glu Asn His Lys Leu Pro
 755 760 765

Ala Glu Pro Leu Glu Lys Pro Ile Met Leu Thr Glu Ser Leu Phe Asn
770 775 780

Gly Ser His Tyr Leu Asp Val Leu Tyr Lys Met Thr Ala Asp Asp Gln
785 790 795 800

Arg Tyr Ser Gly Ser Thr Tyr Leu Ser Asp Pro Arg Leu Thr Ala Asn
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820 825 830

Leu Glu Ile Glu Gly Met Ala Asn Cys Leu Pro Phe Tyr Gly Val Ala
835 840 845

Asp Leu Lys Glu Ile Leu Asn Ala Ile Leu Asn Arg Asn Ala Lys Glu
850 855 860

Val Tyr Glu Cys Arg Pro Arg Lys Val Ile Ser Tyr Leu Glu Gly Glu
865 870 875 880

Ala Val Arg Leu Ser Arg Gln Leu Pro Met Tyr Leu Ser Lys Glu Asp
885 890 895

Ile Gln Asp Ile Ile Tyr Arg Met Lys His Gln Phe Gly Asn Glu Ile
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Glu Pro Ala Lys Ala Ile Lys Pro Ile Asp Arg Lys Ser Val His Gln

99

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att tgc tct ggg cag gtg gta ctg agt cta agc act gcg gta aag gag				147
Ile Cys Ser Gly	Gln Val Val Leu Ser	Leu Ser Thr Ala Val	Lys Glu	
30	35	40		
tta gta gaa aac agt ctg gat gct ggt gcc act aat att gat cta aag				195
Leu Val Glu Asn Ser Leu Asp	Ala Gly Ala Thr Asn Ile Asp	Leu Lys		
45	50	55		
ctt aag gac tat gga gtg gat ctt att gaa gtt tca gac aat gga tgt				243
Leu Lys Asp Tyr Gly Val Asp	Leu Ile Glu Val Ser Asp Asn Gly Cys			
60	65	70		
ggg gta gaa gaa gaa aac ttc gaa ggc tta act ctg aaa cat cac aca				291
Gly Val Glu Glu Glu Asn Phe	Glu Gly Leu Thr Leu Lys His His Thr			
75	80	85		
tct aag att caa gag ttt gcc gac cta act cag gtt gaa act ttt ggc				339
Ser Lys Ile Gln Glu Phe Ala Asp	Leu Thr Gln Val Glu Thr Phe Gly			
90	95	100	105	
ttt cgg ggg gaa gct ctg agc tca ctt tgt gca ctg agc gat gtc acc				387
Phe Arg Gly Glu Ala Leu Ser Ser Leu Cys Ala Leu Ser Asp Val Thr				
110	115	120		
att tct acc tgc cac gca tcg gcg aag gtt gga act cga ctg atg ttt				435
Ile Ser Thr Cys His Ala Ser Ala Lys Val Gly Thr Arg Leu Met Phe				
125	130	135		
gat cac aat ggg aaa att atc cag aaa acc ccc tac ccc cgc ccc aga				483
Asp His Asn Gly Lys Ile Ile Gln Lys Thr Pro Tyr Pro Arg Pro Arg				
140	145	150		
ggg acc aca gtc agc gtg cag cag tta ttt tcc aca cta cct gtg cgc				531
Gly Thr Thr Val Ser Val Gln Gln Leu Phe Ser Thr Leu Pro Val Arg				
155	160	165		
cat aag gaa ttt caa agg aat att aag aag gag tat gcc aaa atg gtc				579
His Lys Glu Phe Gln Arg Asn Ile Lys Lys Glu Tyr Ala Lys Met Val				
170	175	180	185	
cag gtc tta cat gca tac tgt atc att tca gca ggc atc cgt gta agt				627
Gln Val Leu His Ala Tyr Cys Ile Ile Ser Ala Gly Ile Arg Val Ser				
190	195	200		
tgc acc aat cag ctt gga caa gga aaa cga cag cct gtg gta tgc aca				675
Cys Thr Asn Gln Leu Gly Gln Gly Lys Arg Gln Pro Val Val Cys Thr				
205	210	215		
ggt gga agc ccc agc ata aag gaa aat atc ggc tct gtg ttt ggg cag				723
Gly Gly Ser Pro Ser Ile Lys Glu Asn Ile Gly Ser Val Phe Gly Gln				
220	225	230		
aag cag ttg caa agc ctc att cct ttt gtt cag ctg ccc cct agt gac				771
Lys Gln Leu Gln Ser Leu Ile Pro Phe Val Gln Leu Pro Pro Ser Asp				
235	240	245		
tcc gtg tgt gaa gag tac ggt ttg agc tgt tcg gat gct ctg cat aat				819
Ser Val Cys Glu Glu Tyr Gly Leu Ser Cys Ser Asp Ala Leu His Asn				

250	255	260	265	
ctt ttt tac atc tca ggt ttc att tca caa tgc acg cat gga gtt gga				867
Leu Phe Tyr Ile Ser Gly Phe Ile Ser Gln Cys Thr His Gly Val Gly	270	275	280	
agg agt tca aca gac aga cag ttt ttc ttt atc aac cgg cgg cct tgt				915
Arg Ser Ser Thr Asp Arg Gln Phe Phe Phe Ile Asn Arg Arg Pro Cys	285	290	295	
gac cca gca aag gtc tgc aga ctc gtg aat gag gtc tac cac atg tat				963
Asp Pro Ala Lys Val Cys Arg Leu Val Asn Glu Val Tyr His Met Tyr	300	305	310	
aat cga cac cag tat cca ttt gtt gtt ctt aac att tct gtt gat tca				1011
Asn Arg His Gln Tyr Pro Phe Val Val Leu Asn Ile Ser Val Asp Ser	315	320	325	
gaa tgc gtt gat atc aat gtt act cca gat aaa agg caa att ttg cta				1059
Glu Cys Val Asp Ile Asn Val Thr Pro Asp Lys Arg Gln Ile Leu Leu	330	335	340	345
caa gag gaa aag ctt ttg ttg gca gtt tta aag acc tct ttg ata gga				1107
Gln Glu Glu Lys Leu Leu Leu Ala Val Leu Lys Thr Ser Leu Ile Gly	350	355	360	
atg ttt gat agt gat gtc aac aag cta aat gtc agt cag cag cca ctg				1155
Met Phe Asp Ser Asp Val Asn Lys Leu Asn Val Ser Gln Gln Pro Leu	365	370	375	
ctg gat gtt gaa ggt aac tta ata aaa atg cat gca gcg gat ttg gaa				1203
Leu Asp Val Glu Gly Asn Leu Ile Lys Met His Ala Ala Asp Leu Glu	380	385	390	
aag ccc atg gta gaa aag cag gat caa tcc cct tca tta agg act gga				1251
Lys Pro Met Val Glu Lys Gln Asp Gln Ser Pro Ser Leu Arg Thr Gly	395	400	405	
gaa gaa aaa aaa gac gtg tcc att tcc aga ctg cga gag gcc ttt tct				1299
Glu Glu Lys Lys Asp Val Ser Ile Ser Arg Leu Arg Glu Ala Phe Ser	410	415	420	425
ctt cgt cac aca aca gag aac aag cct cac agc cca aag act cca gaa				1347
Leu Arg His Thr Thr Glu Asn Lys Pro His Ser Pro Lys Thr Pro Glu	430	435	440	
cca aga agg agc cct cta gga cag aaa agg ggt atg ctg tct tct agc				1395
Pro Arg Arg Ser Pro Leu Gly Gln Lys Arg Gly Met Leu Ser Ser Ser	445	450	455	
act tca ggt gcc atc tct gac aaa ggc gtc ctg aga cct cag aaa gag				1443
Thr Ser Gly Ala Ile Ser Asp Lys Gly Val Leu Arg Pro Gln Lys Glu	460	465	470	
gca gtg agt tcc agt cac gga ccc agt gac cct acg gac aga gcg gag				1491
Ala Val Ser Ser Ser His Gly Pro Ser Asp Pro Thr Asp Arg Ala Glu	475	480	485	
gtg gag aag gac tcg ggg cac ggc agc act tcc gtg gat tct gag ggg				1539
Val Glu Lys Asp Ser Gly His Gly Ser Thr Ser Val Asp Ser Glu Gly				

490		495		500		505	
ttc agc atc cca gac acg ggc agt cac tgc agc agc gag tat gcg gcc							1587
Phe Ser Ile Pro Asp Thr Gly Ser His Cys Ser Ser Glu Tyr Ala Ala							
		510		515		520	
agc tcc cca ggg gac agg ggc tgc cag gaa cat gtg gac tct cag gag							1635
Ser Ser Pro Gly Asp Arg Gly Ser Gln Glu His Val Asp Ser Gln Glu							
		525		530		535	
aaa gcg cct gaa act gac gac tct ttt tca gat gtg gac tgc cat tca							1683
Lys Ala Pro Glu Thr Asp Asp Ser Phe Ser Asp Val Asp Cys His Ser							
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gac cag gaa gat acc gga tgt aaa ttt cga gtt ttg cct cag cca act							1731
Asn Gln Glu Asp Thr Gly Cys Lys Phe Arg Val Leu Pro Gln Pro Thr							
		555		560		565	
aat ctc gca acc cca aac aca aag cgt ttt aaa aaa gaa gaa att ctt							1779
Asn Leu Ala Thr Pro Asn Thr Lys Arg Phe Lys Lys Glu Glu Ile Leu							
		570		575		580	585
tcc agt tct gac att tgt caa aag tta gta aat act cag gac atg tca							1827
Ser Ser Ser Asp Ile Cys Gln Lys Leu Val Asn Thr Gln Asp Met Ser							
		590		595		600	
gcc tct cag gtt gat gta gct gtg aaa att aat aag aaa gtt gtg ccc							1875
Ala Ser Gln Val Asp Val Ala Val Lys Ile Asn Lys Lys Val Val Pro							
		605		610		615	
ctg gac ttt tct atg agt tct tta gct aaa cga ata aag cag tta cat							1923
Leu Asp Phe Ser Met Ser Ser Leu Ala Lys Arg Ile Lys Gln Leu His							
		620		625		630	
cat gaa gca cag caa agt gaa ggg gaa cag aat tac agg aag ttt agg							1971
His Glu Ala Gln Gln Ser Glu Gly Glu Gln Asn Tyr Arg Lys Phe Arg							
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gca aag att tgt cct gga gaa aat caa gca gcc gaa gat gaa cta aga							2019
Ala Lys Ile Cys Pro Gly Glu Asn Gln Ala Ala Glu Asp Glu Leu Arg							
		650		655		660	665
aaa gag ata agt aaa acg atg ttt gca gaa atg gaa atc att ggt cag							2067
Lys Glu Ile Ser Lys Thr Met Phe Ala Glu Met Glu Ile Ile Gly Gln							
		670		675		680	
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Phe Asn Leu Gly Phe Ile Ile Thr Lys Leu Asn Glu Asp Ile Phe Ile							
		685		690		695	
gtg gac cag cat gcc acg gac gag aag tat aac ttc gag atg ctg cag							2163
Val Asp Gln His Ala Thr Asp Glu Lys Tyr Asn Phe Glu Met Leu Gln							
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cag cac acc gtg ctc cag ggg cag agg ctc ata gca cct cag act ctc							2211
Gln His Thr Val Leu Gln Gly Gln Arg Leu Ile Ala Pro Gln Thr Leu							
		715		720		725	
aac tta act gct gtt aat gaa gct gtt ctg ata gaa aat ctg gaa ata							2259
Asn Leu Thr Ala Val Asn Glu Ala Val Leu Ile Glu Asn Leu Glu Ile							

730	735	740	745	
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Phe Arg Lys Asn Gly Phe Asp Phe Val Ile Asp Glu Asn Ala Pro Val				
750		755	760	
act gaa agg gct aaa ctg att tcc ttg cca act agt aaa aac tgg acc				2355
Thr Glu Arg Ala Lys Leu Ile Ser Leu Pro Thr Ser Lys Asn Trp Thr				
765		770	775	
ttc gga ccc cag gac gtc gat gaa ctg atc ttc atg ctg agc gac agc				2403
Phe Gly Pro Gln Asp Val Asp Glu Leu Ile Phe Met Leu Ser Asp Ser				
780		785	790	
cct ggg gtc atg tgc cgg cct tcc cga gtc aag cag atg ttt gcc tcc				2451
Pro Gly Val Met Cys Arg Pro Ser Arg Val Lys Gln Met Phe Ala Ser				
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aga gcc tgc cgg aag tcg gtg atg att ggg act gct ctt aac aca agc				2499
Arg Ala Cys Arg Lys Ser Val Met Ile Gly Thr Ala Leu Asn Thr Ser				
810		815	820	825
gag atg aag aaa ctg atc acc cac atg ggg gag atg gac cac ccc tgg				2547
Glu Met Lys Lys Leu Ile Thr His Met Gly Glu Met Asp His Pro Trp				
830		835	840	
aac tgt ccc cat gga agg cca acc atg aga cac atc gcc aac ctg ggt				2595
Asn Cys Pro His Gly Arg Pro Thr Met Arg His Ile Ala Asn Leu Gly				
845		850	855	
gtc att tct cag aac tga ccgtagtcac tgtatggaat aattggtttt				2643
Val Ile Ser Gln Asn				
860				
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			20					25					30		

Leu	Ser	Leu	Ser	Thr	Ala	Val	Lys	Glu	Leu	Val	Glu	Asn	Ser	Leu	Asp
		35					40					45			

Ala Gly Ala Thr Asn Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp
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Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe
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Glu Gly Leu Thr Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala
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Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser
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Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Ala Ser
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Ala Lys Val Gly Thr Arg Leu Met Phe Asp His Asn Gly Lys Ile Ile
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Gln Lys Thr Pro Tyr Pro Arg Pro Arg Gly Thr Thr Val Ser Val Gln
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Gln Leu Phe Ser Thr Leu Pro Val Arg His Lys Glu Phe Gln Arg Asn
 165 170 175

Ile Lys Lys Glu Tyr Ala Lys Met Val Gln Val Leu His Ala Tyr Cys
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Ile Ile Ser Ala Gly Ile Arg Val Ser Cys Thr Asn Gln Leu Gly Gln
 195 200 205

Gly Lys Arg Gln Pro Val Val Cys Thr Gly Gly Ser Pro Ser Ile Lys
 210 215 220

Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile
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Pro Phe Val Gln Leu Pro Pro Ser Asp Ser Val Cys Glu Glu Tyr Gly
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Leu Ser Cys Ser Asp Ala Leu His Asn Leu Phe Tyr Ile Ser Gly Phe
 260 265 270

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Phe Phe Phe Ile Asn Arg Arg Pro Cys Asp Pro Ala Lys Val Cys Arg
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Leu Val Asn Glu Val Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe
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Val Val Leu Asn Ile Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val
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Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu
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Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Val Asn
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Lys Leu Asn Val Ser Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu
 370 375 380

Ile Lys Met His Ala Ala Asp Leu Glu Lys Pro Met Val Glu Lys Gln
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Asp Gln Ser Pro Ser Leu Arg Thr Gly Glu Glu Lys Lys Asp Val Ser
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Gln Lys Arg Gly Met Leu Ser Ser Ser Thr Ser Gly Ala Ile Ser Asp
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595 600 605

Val Lys Ile Asn Lys Lys Val Val Pro Leu Asp Phe Ser Met Ser Ser
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625 630 635 640

Gly Glu Gln Asn Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu
645 650 655

Asn Gln Ala Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Thr Met
660 665 670

Phe Ala Glu Met Glu Ile Ile Gly Gln Phe Asn Leu Gly Phe Ile Ile
675 680 685

Thr Lys Leu Asn Glu Asp Ile Phe Ile Val Asp Gln His Ala Thr Asp
690 695 700

Glu Lys Tyr Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Gly
705 710 715 720

Gln Arg Leu Ile Ala Pro Gln Thr Leu Asn Leu Thr Ala Val Asn Glu
725 730 735

Ala Val Leu Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp
740 745 750

Phe Val Ile Asp Glu Asn Ala Pro Val Thr Glu Arg Ala Lys Leu Ile
755 760 765

Ser Leu Pro Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Val Asp
770 775 780

Glu Leu Ile Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro
785 790 795 800

Ser Arg Val Lys Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val
805 810 815

Met Ile Gly Thr Ala Leu Asn Thr Ser Glu Met Lys Lys Leu Ile Thr
820 825 830

His Met Gly Glu Met Asp His Pro Trp Asn Cys Pro His Gly Arg Pro
835 840 845

Thr Met Arg His Ile Ala Asn Leu Gly Val Ile Ser Gln Asn
850 855 860

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<220>
<223> hMLH1 sense primer

<400> 7
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<210> 8
<211> 19
<212> DNA
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<220>
<223> hMLH1 sense primer

<400> 8
tcgtggcagg ggattattcg 19

<210> 9
<211> 19
<212> DNA
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<220>
<223> hMLH1 sense primer

<400> 9
ctaccaatg cctcaaccg 19

<210> 10
<211> 22
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<220>
<223> hMLH1 sense primer

<400> 10
gagaactgat agaaattgga tg

22

<210> 11
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<223> hMLH1 sense primer

<400> 11
gggacatgag gttctcgc

18

<210> 12
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<400> 12
gggctgtgtg aatcctcag

19

<210> 13
<211> 20
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<223> hMLH1 antisense primer

<400> 13
cggttcacca ctgtctcgtc

20

<210> 14
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<400> 14
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18

<210> 15
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<212> DNA
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<220>
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<400> 15
caagtctctgg tagcaaagtc

20

<210> 16
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
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<400> 16
atggcaaggt caaagagcg

19

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<400> 17
caacaatgta ttcagnaagt cc

22

<210> 18
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<220>
<223> hMLH1 antisense primer

<400> 18
ttgatacaac actttgtatc g

21

<210> 19
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<220>

<223> hMLH1 antisense primer

<400> 19
ggaatactat cagaaggcaa g 21

<210> 20
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<220>
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<400> 20
acagagcaag ttactcagat g 21

<210> 21
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<400> 21
gtacacaatg caggcattag 20

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<400> 22
aatgtggatg ttaatgtgca c 21

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<400> 23
ctgacctcgt cttcctac 18

<210> 24
<211> 19
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<220>

<223> hMLH1 sense primer

<400> 24

cagcaagatg aggagatgc

19

<210> 25

<211> 21

<212> DNA

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<220>

<223> hMLH1 sense primer

<400> 25

ggaaatggtg gaagatgatt c

21

<210> 26

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> hMLH1 sense primer

<400> 26

cttctcaaca ccaagc

16

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> hMLH1 sense primer

<400> 27

gaaattgatg aggaagggaa c

21

<210> 28

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> hMLH1 sense primer

<400> 28

cttctgattg acaactatgt gc

22

<210> 29

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> hMLH1 sense primer
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 cacagaagat ggaaatatcc tg 22

 <210> 30
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 gtgttggtag cacttaagac 20

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 <210> 32
 <211> 19
 <212> DNA
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 <400> 32
 gtaacatgag ccacatggc 19

 <210> 33
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 <400> 33
 ccactgtctc gtccagccg 19

 <210> 34
 <211> 26
 <212> DNA
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<223> hMLH1 5' primer with BamHI restriction site

<400> 34
cgggatccat gtcgttcgtg gcaggg 26

<210> 35
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH1 3' primer with XbaI restriction site

<400> 35
gctctagatt aacacctctc aaagac 26

<210> 36
<211> 21
<212> DNA
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<220>
<223> hMLH1 primer useful for amplifying codons 1 to 394

<400> 36
gcattctagac gtttccttgg c 21

<210> 37
<211> 20
<212> DNA
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<220>
<223> primer useful for amplifying codons 1 to 394 of hMLH1

<400> 37
catccaagct tctgttcccg 20

<210> 38
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 326 to 729 of hMLH1

<400> 38
ggggtgcagc agcacatcg 19

<210> 39
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> primer useful for amplifying codons 326 to 729 of hMLH1
 <400> 39
 ggaggcagaa tgtgtgagcg 20

 <210> 40
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer useful for amplifying codons 602 to 756 plus 128
 nucleotides of 3' untranslated sequence of hMLH1
 <400> 40
 tcccaaagaa ggacttgct 19

 <210> 41
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer useful for amplifying codons 602 to 756 plus 128
 nucleotides of 3' untranslated sequence of hMLH1
 <400> 41
 agtataagtc ttaagtgcta cc 22

 <210> 42
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer useful for amplifying codons 578 to 632 of hMLH1
 <400> 42
 tttatggttt ctcacctgcc 20

 <210> 43
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 43
 gttatctgcc cacctcagc 19

 <210> 44
 <211> 59
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer useful for amplifying codons 1 to 394 of hMLH1 wherein PCR product may be used for coupled transcription-translation

<400> 44
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<210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer useful for amplifying codons 1 to 394 of hMLH1 wherein PCR product may be used for coupled transcription-translation

<400> 45
 catccaagcttctgttcccg 20

<210> 46
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 46
 ggatcctaatacgcactcactatagggagaccaccatgggggtgcagcagcacatcg 56

<210> 47
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 47
 ggaggcagaa tgtgtgagcg 20

<210> 48
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hMLH2 5' primer with a BamHI restriction site

<400> 48
 cgggatccatgaaacaattgcctgcggc 28

<210> 49
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH2 3' primer with XbaI restriction site

<400> 49
gctctagacc agactcatgc tgtttt

26

<210> 50
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH3 5' primer with a BamHI restriction site

<400> 50
cgggatccat ggagcgagct gagagc

26

<210> 51
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH3 3' primer with XbaI restriction site

<400> 51
gctctagagt gaagactctg tct

23

<210> 52
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH2 primer

<400> 52
aagctgctct gttaaaagcg

20

<210> 53
<211> 18
<212> DNA
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<220>
<223> hMLH2 primer

<400> 53
gcaccagcat ccaaggag

18

<210> 54
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH3 primer

<400> 54
caaccatgag acacatcgc

19

<210> 55
<211> 20
<212> DNA
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<220>
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<400> 55
aggttagtga agactctgtc

20

<210> 56
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 1 to 500 of hMLH2

<400> 56
ggatcctaatac gactcact atagggagac caccatggaa caattgcctg cgg

53

<210> 57
<211> 18
<212> DNA
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<220>
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<400> 57
cctgctccac tcactctgc

18

<210> 58
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<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 270 to 755 of hMLH2

<400> 58
ggatcctaatac gactcact atagggagac caccatggaa gatattcttaa agttaatccg

60

<210> 59
<211> 21
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<220>
<223> primer useful for amplifying codons 270 to 755 of hMLH2

<400> 59
ggcttcttct actctatatg g 21

<210> 60
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying from codon 485 to the translation
termination site at codon 933 of hMLH2

<400> 60
ggatcctaatac gactcact ataggagac caccatggca ggtcttgaaa actcttcg 58

<210> 61
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying from codon 485 to the translation
termination site at codon 933 of hMLH2

<400> 61
aaaacaagtc agtgaatcct c 21

<210> 62
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<212> DNA
<213> Artificial Sequence

<220>
<223> 3' primer useful for amplifying up to codon 369 of hMLH2

<400> 62
aagcacatct gtttctgctg 20

<210> 63
<211> 20
<212> DNA
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<220>
<223> 3' primer useful for amplifying up to codon 290 of hMLH2

<400> 63
acgagtagat tcctttaggc 20

<210> 64
<211> 19
<212> DNA
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<220>
<223> 3' primer useful for amplifying up to codon 214 of hMLH2

<400> 64
cagaactgac atgagagcc 19

<210> 65
<211> 52
<212> DNA
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<220>
<223> primer useful for amplifying codons 1 to 863 hMLH3

<400> 65
ggatcctaatac gactcact atagggagac caccatggag cgagctgaga gc 52

<210> 66
<211> 20
<212> DNA
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<220>
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<400> 66
aggtagtagtga agactctgtc 20

<210> 67
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<220>
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<400> 67
ctgaggtctc agcaggc 17

<210> 68
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 415 to 863 of hMLH3

<400> 68
ggatcctaatac gactcact atagggagac caccatgggtg tccattttcca gactgcg 57

<210> 69
<211> 20
<212> DNA
<213> Artificial Sequence

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<400> 69
aggttagtga agactctgtc

20

<210> 70
<211> 21
<212> DNA
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<220>
<223> primer useful for amplifying codons 195 to 233 of hMLH2

<400> 70
ttatttgga gaaaagcaga g

21

<210> 71
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 195 to 233 of hMLH2

<400> 71
ttaaaagact aacctcttgc c

21

<210> 72
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> sequencing primer useful for sequencing codons 195 to 233 of hMLH2

<400> 72
ctgctgttat gaacaatatg g

21

<210> 73
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 233 to 257 of hMLH3

<400> 73

cagaagcagt tgcaaagcc
19

<210> 74
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<400> 74
aaaccgtact cttcacacac 20

<210> 75
<211> 20
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<220>
<223> primer useful for amplifying codons 347 of 377 of hMLH3

<400> 75
gaggaaaagc ttttgttggc 20

<210> 76
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<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 347 of 377 of hMLH3

<400> 76
cagtggctgc tgactgac 18

<210> 77
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 439 to 472 of hMLH3

<400> 77
tccagaacca agaaggagc 19

<210> 78
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 439 to 472 of hMLH3

<400> 78
tgaggtctca gcaggc

16

A handwritten signature or set of initials, possibly 'AK', written in black ink.A small, faint handwritten mark or scribble, possibly a heart shape or a small 'v'.